UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/786,501	02/25/2004	Susan L. Acton	MPI98-052P1RDV10DV1M	3988

30405 7590 07/05/2007

MILLENNIUM PHARMACEUTICALS, INC.
40 Landsdowne Street
CAMBRIDGE, MA 02139

EXAMINER	
SANG, HONG	
ART UNIT	**PAPER NUMBER**
1643	
MAIL DATE	**DELIVERY MODE**
07/05/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Interview Summary	Application No.	Applicant(s)	
	10/786,501	ACTON, SUSAN L.	
	Examiner	Art Unit	
	Hong Sang	1643	

All participants (applicant, applicant's representative, PTO personnel):

(1) *Hong Sang*. (3)_____.

(2) *Mario Cloutier*. (4)_____.

Date of Interview: *25 June 2007*.

Type: a)☒ Telephonic b)☐ Video Conference
c)☐ Personal [copy given to: 1)☐ applicant 2)☐ applicant's representative]

Exhibit shown or demonstration conducted: d)☐ Yes e)☐ No.
If Yes, brief description: _____.

Claim(s) discussed: _____.

Identification of prior art discussed: _____.

Agreement with respect to the claims f)☐ was reached. g)☐ was not reached. h)☒ N/A.

Substance of Interview including description of the general nature of what was agreed to if an agreement was reached, or any other comments: *see continuation sheet*.

(A fuller description, if necessary, and a copy of the amendments which the examiner agreed would render the claims allowable, if available, must be attached. Also, where no copy of the amendments that would render the claims allowable is available, a summary thereof must be attached.)

THE FORMAL WRITTEN REPLY TO THE LAST OFFICE ACTION MUST INCLUDE THE SUBSTANCE OF THE INTERVIEW. (See MPEP Section 713.04). If a reply to the last Office action has already been filed, APPLICANT IS GIVEN A NON-EXTENDABLE PERIOD OF THE LONGER OF ONE MONTH OR THIRTY DAYS FROM THIS INTERVIEW DATE, OR THE MAILING DATE OF THIS INTERVIEW SUMMARY FORM, WHICHEVER IS LATER, TO FILE A STATEMENT OF THE SUBSTANCE OF THE INTERVIEW. See Summary of Record of Interview requirements on reverse side or on attached sheet.

Examiner Note: You must sign this form unless it is an Attachment to a signed Office action.

_____
Examiner's signature, if required

Summary of Record of Interview Requirements

Manual of Patent Examining Procedure (MPEP), Section 713.04, Substance of Interview Must be Made of Record
A complete written statement as to the substance of any face-to-face, video conference, or telephone interview with regard to an application must be made of record in the application whether or not an agreement with the examiner was reached at the interview.

Title 37 Code of Federal Regulations (CFR) § 1.133 Interviews
Paragraph (b)
In every instance where reconsideration is requested in view of an interview with an examiner, a complete written statement of the reasons presented at the interview as warranting favorable action must be filed by the applicant. An interview does not remove the necessity for reply to Office action as specified in §§ 1.111, 1.135. (35 U.S.C. 132)

37 CFR §1.2 Business to be transacted in writing.
All business with the Patent or Trademark Office should be transacted in writing. The personal attendance of applicants or their attorneys or agents at the Patent and Trademark Office is unnecessary. The action of the Patent and Trademark Office will be based exclusively on the written record in the Office. No attention will be paid to any alleged oral promise, stipulation, or understanding in relation to which there is disagreement or doubt.

The action of the Patent and Trademark Office cannot be based exclusively on the written record in the Office if that record is itself incomplete through the failure to record the substance of interviews.

It is the responsibility of the applicant or the attorney or agent to make the substance of an interview of record in the application file, unless the examiner indicates he or she will do so. It is the examiner's responsibility to see that such a record is made and to correct material inaccuracies which bear directly on the question of patentability.

Examiners must complete an Interview Summary Form for each interview held where a matter of substance has been discussed during the interview by checking the appropriate boxes and filling in the blanks. Discussions regarding only procedural matters, directed solely to restriction requirements for which interview recordation is otherwise provided for in Section 812.01 of the Manual of Patent Examining Procedure, or pointing out typographical errors or unreadable script in Office actions or the like, are excluded from the interview recordation procedures below. Where the substance of an interview is completely recorded in an Examiners Amendment, no separate Interview Summary Record is required.

The Interview Summary Form shall be given an appropriate Paper No., placed in the right hand portion of the file, and listed on the "Contents" section of the file wrapper. In a personal interview, a duplicate of the Form is given to the applicant (or attorney or agent) at the conclusion of the interview. In the case of a telephone or video-conference interview, the copy is mailed to the applicant's correspondence address either with or prior to the next official communication. If additional correspondence from the examiner is not likely before an allowance or if other circumstances dictate, the Form should be mailed promptly after the interview rather than with the next official communication.

The Form provides for recordation of the following information:
- Application Number (Series Code and Serial Number)
- Name of applicant
- Name of examiner
- Date of interview
- Type of interview (telephonic, video-conference, or personal)
- Name of participant(s) (applicant, attorney or agent, examiner, other PTO personnel, etc.)
- An indication whether or not an exhibit was shown or a demonstration conducted
- An identification of the specific prior art discussed
- An indication whether an agreement was reached and if so, a description of the general nature of the agreement (may be by attachment of a copy of amendments or claims agreed as being allowable). Note: Agreement as to allowability is tentative and does not restrict further action by the examiner to the contrary.
- The signature of the examiner who conducted the interview (if Form is not an attachment to a signed Office action)

It is desirable that the examiner orally remind the applicant of his or her obligation to record the substance of the interview of each case. It should be noted, however, that the Interview Summary Form will not normally be considered a complete and proper recordation of the interview unless it includes, or is supplemented by the applicant or the examiner to include, all of the applicable items required below concerning the substance of the interview.

A complete and proper recordation of the substance of any interview should include at least the following applicable items:
1) A brief description of the nature of any exhibit shown or any demonstration conducted,
2) an identification of the claims discussed,
3) an identification of the specific prior art discussed,
4) an identification of the principal proposed amendments of a substantive nature discussed, unless these are already described on the Interview Summary Form completed by the Examiner,
5) a brief identification of the general thrust of the principal arguments presented to the examiner,
   (The identification of arguments need not be lengthy or elaborate. A verbatim or highly detailed description of the arguments is not required. The identification of the arguments is sufficient if the general nature or thrust of the principal arguments made to the examiner can be understood in the context of the application file. Of course, the applicant may desire to emphasize and fully describe those arguments which he or she feels were or might be persuasive to the examiner.)
6) a general indication of any other pertinent matters discussed, and
7) if appropriate, the general results or outcome of the interview unless already described in the Interview Summary Form completed by the examiner.

Examiners are expected to carefully review the applicant's record of the substance of an interview. If the record is not complete and accurate, the examiner will give the applicant an extendable one month time period to correct the record.

Examiner to Check for Accuracy

If the claims are allowable for other reasons of record, the examiner should send a letter setting forth the examiner's version of the statement attributed to him or her. If the record is complete and accurate, the examiner should place the indication, "Interview Record OK" on the paper recording the substance of the interview along with the date and the examiner's initials.

Examiner called applicants' representative Mario Cloutier regarding submitting a paper copy of sequence listing and a statement that the paper copy and the CRF are identical and that no new matter has been introduced. Applicants faxed the following documents to the examiner.

1. paper copy of sequence listing.
2. a statement that the paper copy and the CRF are identical and that no new matter has been introduced.

See attached fax documents.

Hong Sang, Ph.D.
Art Unit 1643
June 25, 2007

In re application of:	Susan L. Acton		
Application No.:	10/786,501	Group No.:	1643
Filed:	February 25, 2004	Examiner:	SANG, HONG
For:	CARDIOVASCULAR SYSTEM ASSOCIATED PROTEIN KINASE 3 (CSAPK-3) ANTIBODIES (as amended)		

Practitioner's Docket No. MPI98-052P1RDV10DV1M ***PATENT***

Certificate of Transmission under 37 CFR 1.8

1-571-273 8145

I hereby certify that this correspondence is being facsimiled transmitted to the United States Patent and Trademark Office

on June 25, 2007.

Ann Sherry

Signature

Ann Sherry

Typed or printed name of person signing Certificate

Note: Each paper must have its own certificate of transmission, or this certificate must identify each submitted paper.

Submitted herewith:

This Certificate of Transmission under 37 CFR 1.8	1 page
Submission of Sequence Listing	4 pages
Paper Copy of Sequence Listing	31 pages
Total (including Fax Transmittal)	36 pages

Practitioner's Docket No. MPI98-052P1RDV10DV1M *PATENT*

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:	Susan L. Acton		
Application No.:	10/786,501	Group No.:	1643
Filed:	February 25, 2004	Examiner:	SANG, HONG
For:	CARDIOVASCULAR SYSTEM ASSOCIATED PROTEIN KINASE 3 (CSAPK-3) ANTIBODIES (as amended)		

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

SUBMISSION OF "SEQUENCE LISTING," COMPUTER READABLE COPY, AND/OR AMENDMENT PERTAINING THERETO FOR BIOTECHNOLOGY INVENTION CONTAINING NUCLEOTIDE AND/OR AMINO ACID SEQUENCE

1. This submission accompanies the new application being filed concurrently herewith

IDENTIFICATION OF PERSON MAKING STATEMENT

2. I, Mario Cloutier
(type or print name of person signing below)

state the following:

CERTIFICATION UNDER 37 C.F.R. SECTIONS 1.8(a) and 1.10*

I hereby certify that, on the date shown below, this correspondence is being:

MAILING

☐ deposited with the United States Postal Service in an envelope addressed to: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

37 C.F.R. SECTION 1.8(a) **37 C.F.R. SECTION 1.10***

☐ with sufficient postage as first class mail. ☐ as "Express Mail Post Office to Addressee" Mailing Label No.

TRANSMISSION

☒ transmitted by facsimile to the Patent and Trademark Office at 1-571-273 8145.

Signature Ann Sherry

Date: June 25, 2007

Ann Sherry
(type or print name of person certifying)

***WARNING:** *Each paper or fee filed by "Express Mail" must have the number of the "Express Mail" mailing label placed thereon prior to mailing. 37 C.F.R. section 1.10(b). "Since the filing of correspondence under section 1.10 without the Express Mail mailing label thereon is an oversight that can be avoided by the exercise of reasonable care, requests for waiver of this requirement will not be granted on petition." Notice of Oct. 24, 1996, 60 Fed. Reg. 56,439, at 56,442.*

Practitioner's Docket No. MPI98-052P1RDV10DV1M

ITEMS BEING SUBMITTED

3. Submitted herewith are:

A. [ ] "Sequence Listing(s)" for the nucleotide and/or amino acid sequence(s) in this application. Each sequence in the "Sequence Listing" is assigned a separate identifier as required in 37 C.F.R. Section 1.821(c) and 37 C.F.R. Sections 1.822 and 1.823.

B. [ ] An amendment to the description and/or claims, wherein reference is made to the sequence by use of the assigned identifier, as required in 37 C.F.R. Section 1.821(d).

C. [ ] A copy of each "Sequence Listing" submitted for this application in computer readable form, in accordance with the requirements of 37 C.F.R. Sections 1.821(e) and 1.824.

D. [X] Paper copy of "Sequence Listing" corresponding to the electronic copy of "Sequence Listing" on file in present application.

In re application of:			
Application No.:			
Filed:			
For:			

The Computer readable form(s) of applicant's other application corresponds to the "Sequence Identifier(s)" of the application as follows:

Computer Readable Form (other application)	"Sequence Identifier" (this application)

E. [X] A statement that the content of each "Sequence Listing" submitted and each computer readable copy are the same, as required in 37 C.F.R. Section 1.821(g).

[ ] Because the statement is not made by a person registered to practice before the Office, the Statement is verified as required in 37 C.F.R. Section 1.821(b).

F. [ ] Because this submission is made in fulfilling the requirement under 37 C.F.R. Section 1.821(g), a statement that the submission includes no new matter.

[ ] Because the statement is not made by a person registered to practice before the Office, the statement is verified, as required in 37 C.F.R. Section 1.821(g).

Practitioner's Docket No. MPI98-052P1RDV10DV1M

STATEMENTS REGARDING THE SEQUENCE LISTING SUBMITTED HEREWITH

4. I hereby state:

A. [X] Each computer readable form submitted in this application, including those forms requested to be transferred from applicant's other application, is the same as the "Sequence Listing" to which it is indicated to relate.

B. [X] All papers accompanying this submission, or for which a request for transfer from applicants' other application, introduce no new matter.

EXTENSION OF TERM

5. The proceedings herein are for a patent application and the provisions of 37 C.F.R. Section 1.136 apply.

(a) [ ] Applicant petitions for an extension of time under 37 C.F.R. Section 1.136 (fees: 37 C.F.R. Section 1.17(a)(1)-(4)) for the total number of months checked below:

Extension (months)	Fee for other than small entity	Fee for small entity
[ ] one month	$ 120.00	$ 60.00
[ ] two months	$ 450.00	$ 225.00
[ ] three months	$1,020.00	$ 510.00
[ ] four months	$1,590.00	$ 795.00

Fee $0.00

If an additional extension of time is required, please consider this a petition therefor.

[ ] An extension for _____ months has already been secured, and the fee paid therefor of $0.00 is deducted from the total fee due for the total months of extension now requested.

Extension fee due with this request $0.00

OR

(b) [X] Applicant believes that no extension of term is required. However, this conditional petition is being made to provide for the possibility that applicant has inadvertently overlooked the need for a petition and fee for extension of time.

Practitioner's Docket No. MPI98-052P1RDV10DV1M

FEE PAYMENT

6. [ ] Attached is a check in the sum of $_____.

[ ] Charge Account No. _____ the sum of $0.00 .
A duplicate of this transmittal is attached.

FEE DEFICIENCY

7. [ ] If any additional extension and/or fee is required, charge Account No._____.

8. Correspondence Address
Direct all future correspondence to:

Customer Number 30405
OR
Intellectual Property Department
MILLENNIUM PHARMACEUTICALS, INC.
40 Landsdowne Street
Cambridge, MA 02139

June 25, 2007

MILLENNIUM PHARMACEUTICALS, INC.

By _____
Mario Cloutier
Registration No. 57,225
40 Landsdowne Street
Cambridge, MA 02139
Telephone - 617-577-3522
Facsimile - 617-551-8820

SEQUENCE LISTING

<110> Acton, Susan

<120> NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR

<130> MNI-050

<140>
<141>

<160> 15

<170> PatentIn Ver. 2.0

<210> 1
<211> 4137
<212> DNA
<213> Homo sapiens

<220>
<223> 'n' at positions 2872, 3597 and 3682 may be any nucleic acid

<220>
<221> CDS
<222> (297)..(1202)

<400> 1
tcgacccacg cgtccgggag gatcgggagt cgcgggagga tgggccgccg ctaggctcgc 60

actccggacg cgcctcgcag tgcgcagggt gggtgccccg cgcctgcagc gtccgccggg 120

gcggcgcggc gggaggtggc cgacaggctc cgggcctcgc agcctcagcc cccggcccag 180

cgcgctttcc gacggcggcg ccgcgccgag ccacccgccc gcccaaggtc tctcgcgggc 240

gggagaacgg aaaactccca acttcctgag ttctaaagtt cctgttgctt cagaca atg 299
Met
1

gat gag caa tca caa gga atg caa ggg cca cct gtt cct cag ttc caa 347
Asp Glu Gln Ser Gln Gly Met Gln Gly Pro Pro Val Pro Gln Phe Gln
5 10 15

cca cag aag gcc tta cga ccg gat atg ggc tat aat aca tta gcc aac 395
Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala Asn
20 25 30

ttt cga ata gaa aag aaa att ggt cgc gga caa ttt agt gaa gtt tat 443
Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr
35 40 45

aga gca gcc tgt ctc ttg gat gga gta cca gta gct tta aaa aaa gtg 491
Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys Val
50 55 60 65

cag ata ttt gat tta atg gat gcc aaa gca cgt gct gat tgc atc aaa 539

```
Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile Lys
                70                  75                  80

gaa ata gat ctt ctt aag caa ctc aac cat cca aat gta ata aaa tat   587
Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys Tyr
            85                  90                  95

tat gca tca ttc att gaa gat aat gaa cta aac ata gtt ttg gaa cta   635
Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu Leu
        100                 105                 110

gca gat gct ggc gac cta tcc aga atg atc aag cat ttt aag aag caa   683
Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys Gln
    115                 120                 125

aag agg cta att cct gaa aga act gtt tgg aag tat ttt gtt cag ctt   731
Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln Leu
130                 135                 140                 145

tgc agt gca ttg gaa cac atg cat tct cga aga gtc atg cat aga gat   779
Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg Asp
                150                 155                 160

ata aaa cca gct aat gtg ttc att aca gcc act ggg gtg gta aaa ctt   827
Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys Leu
            165                 170                 175

gga gat ctt ggg ctt ggc cgg ttt ttc agc tca aaa acc aca gct gca   875
Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala Ala
        180                 185                 190

cat tct tta gtt ggt acg cct tat tac atg tct cca gag aga ata cat   923
His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His
    195                 200                 205

gaa aat gga tac aac ttc aaa tct gac atc tgg tct ctt ggc tgt cta   971
Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu
210                 215                 220                 225

cta tat gag atg gct gca tta caa agt cct ttc tat ggt gac aaa atg   1019
Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met
                230                 235                 240

aat tta tac tca ctg tgt aag aag ata gaa cag tgt gac tac cca cct   1067
Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro Pro
            245                 250                 255

ctt cct tca gat cac tat tca gaa gaa ctc cga cag tta gtt aat atg   1115
Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn Met
        260                 265                 270

tgc atc aac cca gat cca gag aag cga cca gac gtc acc tat gtt tat   1163
Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val Tyr
    275                 280                 285

gac gta gca aag agg atg cat gca tgc act gca agc agc taaacatgca   1212
Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Ser
```

290 295 300

agatcatgaa gagtgtaacc aaagtaattg aaagtatttt gtgcaaagtc gtacctsccc 1272

atttatgtct gggtgttaag attaatattt cagagctagt gtgctctgaa tccttaacca 1332

gttttcatat aagcttcatt ttgtaccagt cacctaaatc acctccttgc aacccccaaa 1392

tgactttgga ataactgaat tgcatgttag gagagaaaat gaaacatgat ggttttgaat 1452

ggctaaaggt ttatagaatt tcttacagtt ttctgctgat aaattgtgtt tagatagact 1512

gtcagtgcca aatattgaag gtgcagcttg gcacacatca gaatagactc atacctgaga 1572

aaaagtatct gaacatgtga cttgtttctt ttttagtaat ttatggacat tgagatgaac 1632

acaattgtga acttttgtga agattttatt tttaaacgtt tgaagtacta gttttagttc 1692

ttagcagagt agttttcaaa tatgattctt atgataaatg tagacacaaa ctatttgaga 1752

aacatttaga actcttagct tatacattca aaatgtaact attaaatgtg aagatttggg 1812

gacaaaatgt gagtcagaca ctgaagagtt ttttgttttg ttttaatatt tttgatattc 1872

tctttgcatt gaaatggtat aaatgaatcc atttaaaaag tggttaagga tttgtttagc 1932

tggtgtgata ataattttta aagttgcaca ttgcccaagg ctttttttgt gtgtttttat 1992

tgttgtttgt acatttgaaa aatattcttt gaataacctt gcagtactat atttcaagrt 2052

ttctttataa atttaagtgc attttaactc ataattgtac actataatat aagcctaagt 2112

ttttattcat aagttttatt gaagttctga tcggtcccct tcagaaattt ttttatatta 2172

ttcttcaagt tactttctta tttatattgt atgtgcattt tatccattaa tgtttcatac 2232

tttctgagag tataataccc ttttaaaaga tatttggtat accaatactt ttcctggatt 2292

gaaaactttt tttaaacttt ttaaaatttg ggccactctg tatgcatatg tttggtcttg 2352

ttaaagagga agaaaggatg tgtgttatac tgtacctgtg aatgttgata cagttacaat 2412

ttatttgaca aggttgtaat tctagaatat gcttaataaa atgaaaactg gccatgacta 2472

cagccagaac tgttatgaga ttaacatttc tattgagaag cttttgagta aagtactgta 2532

tttgttcatg aagatgactg agatggtaac acttcgtgta gcttaaggaa atgggcagaa 2592

tttcgtaaat gctgttgtgc agatgtgttt tccctgaatg ctttcgtatt agtggcgacc 2652

agtttctcac agaattgtga agcctgaagg ccaagaggaa gtcactgtta aaggactctg 2712

tgccatctta caaccttgga tgaattatcc tgccaacgtg aaaacctcat gttcaaagaa 2772

cacttccctt tagccgatgt aactgctggt tttgtttttc atatgtgttt ttcttacact 2832

catttgaatg ctttcaagca tttgtaaact taaaaaaaan wawaaagggc aaaaagtctg 2892

aacccttgtt ttctgaaatc taatcagtta tgtatggttt ctgaagggta attttatttt 2952

ggaataggta aagcgaaacc tgttttgtcw tgtttttcct gagggctaga tgcatttttt 3012

ttctcacact cttaatgact tttaacattt atactgagca tccatagata tattcctaga 3072

agtatgagaa gaattattct tattgaccat taatgtcatg ttcattttaa tgtaatataa 3132

ttgagatgaa atgttctctg gttggaacag atactctctt ttttttttctt gcaatcttta 3192

agaatacata gatctaaaat tcattagctt gacccctcaa agtaactttt aagtaaagat 3252

taaagctttt cttctcagtg aatatatctg ctagaaggaa atagctggga agaatttaat 3312

gatcagggaa attcattatt tctatatgtg gaaacttttt gcttcgaata ttgtatcttt 3372

ttaaatctaa atgttcatat ttttcctgaa gaaaccactg tgtaaaaatc aaattttaat 3432

tttgaatgga ataatttcaa agaactatga agatgatttg aagctctaat ttatatagtc 3492

acctataaaa tgttctttat atgtgttcat aagtaaattt tatattgatt aagttaaact 3552

tttgaattga tttgaggagc agtaaaatga aagctatatc tattnctaaa ccytatttag 3612

acattggkac cagttaccca ggtgaaaata kggagtaact ttgttttgta tggtaaggtt 3672

taggaatggn ggatgaaggg tatctctata taaataaagt gctcaacaat gtgcaatgat 3732

tgtaaattta gtaagatatt acagccattt catgaatgct ttaccattca acatagtatc 3792

tattacaaaa caccttttctt gtatccatat acttcaggtg ttgctgttaa catttactat 3852

gatatttatt ttaaccaaaa tgttactcac attaaatgtt tattctttaa aatgaatgta 3912

ttatgttttt aacccacaaa tgcatactta ccctgtgcct catatttcaa tagtactgta 3972

atatggacat cttttgtgaa atacttttat tttgttatgc tttaaatata catacaaaaa 4032

gatttctgtt attagctttg aaaattgtat aatatcctaa tataacaaaa atataaaaat 4092

aaaaatgaat acagtaaaaa aaaaaaaaaa aaaaaaaaaa aaagg 4137

<210> 2
<211> 302
<212> PRT
<213> Homo sapiens

<400> 2
Met Asp Glu Gln Ser Gln Gly Met Gln Gly Pro Pro Val Pro Gln Phe
1 5 10 15

Gln Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala
20 25 30

Asn Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val

```
          35                  40                  45

Tyr Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys
     50                  55                  60

Val Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile
 65                  70                  75                  80

Lys Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys
                85                  90                  95

Tyr Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu
            100                 105                 110

Leu Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys
        115                 120                 125

Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln
    130                 135                 140

Leu Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg
145                 150                 155                 160

Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys
                165                 170                 175

Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala
            180                 185                 190

Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile
        195                 200                 205

His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys
    210                 215                 220

Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys
225                 230                 235                 240

Met Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro
                245                 250                 255

Pro Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn
            260                 265                 270

Met Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val
        275                 280                 285

Tyr Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Ser
    290                 295                 300


<210> 3
<211> 906
<212> DNA
<213> Homo sapiens

<220>
```

<221> CDS
<222> (1)..(906)

<400> 3

```
atg gat gag caa tca caa gga atg caa ggg cca cct gtt cct cag ttc   48
Met Asp Glu Gln Ser Gln Gly Met Gln Gly Pro Pro Val Pro Gln Phe
  1               5                  10                  15

caa cca cag aag gcc tta cga ccg gat atg ggc tat aat aca tta gcc   96
Gln Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala
            20                  25                  30

aac ttt cga ata gaa aag aaa att ggt cgc gga caa ttt agt gaa gtt   144
Asn Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val
        35                  40                  45

tat aga gca gcc tgt ctc ttg gat gga gta cca gta gct tta aaa aaa   192
Tyr Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys
    50                  55                  60

gtg cag ata ttt gat tta atg gat gcc aaa gca cgt gct gat tgc atc   240
Val Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile
65                  70                  75                  80

aaa gaa ata gat ctt ctt aag caa ctc aac cat cca aat gta ata aaa   288
Lys Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys
                85                  90                  95

tat tat gca tca ttc att gaa gat aat gaa cta aac ata gtt ttg gaa   336
Tyr Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu
            100                 105                 110

cta gca gat gct ggc gac cta tcc aga atg atc aag cat ttt aag aag   384
Leu Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys
        115                 120                 125

caa aag agg cta att cct gaa aga act gtt tgg aag tat ttt gtt cag   432
Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln
    130                 135                 140

ctt tgc agt gca ttg gaa cac atg cat tct cga aga gtc atg cat aga   480
Leu Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg
145                 150                 155                 160

gat ata aaa cca gct aat gtg ttc att aca gcc act ggg gtg gta aaa   528
Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys
                165                 170                 175

ctt gga gat ctt ggg ctt ggc cgg ttt ttc agc tca aaa acc aca gct   576
Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala
            180                 185                 190

gca cat tct tta gtt ggt acg cct tat tac atg tct cca gag aga ata   624
Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile
        195                 200                 205

cat gaa aat gga tac aac ttc aaa tct gac atc tgg tct ctt ggc tgt   672
```

```
His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys
    210                 215                 220

cta cta tat gag atg gct gca tta caa agt cct ttc tat ggt gac aaa   720
Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys
225                 230                 235                 240

atg aat tta tac tca ctg tgt aag aag ata gaa cag tgt gac tac cca   768
Met Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro
                245                 250                 255

cct ctt cct tca gat cac tat tca gaa gaa ctc cga cag tta gtt aat   816
Pro Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn
            260                 265                 270

atg tgc atc aac cca gat cca gag aag cga cca gac gtc acc tat gtt   864
Met Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val
        275                 280                 285

tat gac gta gca aag agg atg cat gca tgc act gca agc agc           906
Tyr Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Ser
    290                 295                 300


<210> 4
<211> 2120
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (47)..(1411)

<400> 4
gtcgacccac gcgtccggtg gaagtataat actttgtcat tatgag atg tcg tct    55
                                                 Met Ser Ser
                                                   1

ctc ggt gcc tcc ttt gtg caa att aaa ttt gat gac ttg cag ttt ttt   103
Leu Gly Ala Ser Phe Val Gln Ile Lys Phe Asp Asp Leu Gln Phe Phe
      5                  10                  15

gaa aac tgc ggt gga gga agt ttt ggg agt gtt tat cga gcc aaa tgg   151
Glu Asn Cys Gly Gly Gly Ser Phe Gly Ser Val Tyr Arg Ala Lys Trp
 20                  25                  30                  35

ata tca cag gac aag gag gtg gct gta aag aag ctc ctc aaa ata gag   199
Ile Ser Gln Asp Lys Glu Val Ala Val Lys Lys Leu Leu Lys Ile Glu
                 40                  45                  50

aaa gag gca gaa ata ctc agt gtc ctc agt cac aga aac atc atc cag   247
Lys Glu Ala Glu Ile Leu Ser Val Leu Ser His Arg Asn Ile Ile Gln
             55                  60                  65

ttt tat gga gta att ctt gaa cct ccc aac tat ggc att gtc aca gaa   295
Phe Tyr Gly Val Ile Leu Glu Pro Pro Asn Tyr Gly Ile Val Thr Glu
         70                  75                  80
```

```
tat gct tct ctg gga tca ctc tat gat tac att aac agt aac aga agt   343
Tyr Ala Ser Leu Gly Ser Leu Tyr Asp Tyr Ile Asn Ser Asn Arg Ser
     85                  90                  95

gag gag atg gat atg gat cac att atg acc tgg gcc act gat gta gcc   391
Glu Glu Met Asp Met Asp His Ile Met Thr Trp Ala Thr Asp Val Ala
100                 105                 110                 115

aaa gga atg cat tat tta cat atg gag gct cct gtc aag gtg att cac   439
Lys Gly Met His Tyr Leu His Met Glu Ala Pro Val Lys Val Ile His
                120                 125                 130

aga gac ctc aag tca aga aac gtt gtt ata gct gct gat gga gta ctg   487
Arg Asp Leu Lys Ser Arg Asn Val Val Ile Ala Ala Asp Gly Val Leu
            135                 140                 145

aag atc tgt gac ttt ggt gcc tct cgg ttc cat aac cat aca aca cac   535
Lys Ile Cys Asp Phe Gly Ala Ser Arg Phe His Asn His Thr Thr His
        150                 155                 160

atg tcc ttg gtt gga act ttc cca tgg atg gct cca gaa gtt atc cag   583
Met Ser Leu Val Gly Thr Phe Pro Trp Met Ala Pro Glu Val Ile Gln
    165                 170                 175

agt ctc cct gtg tca gaa act tgt gac aca tat tcc tat ggt gtg gtt   631
Ser Leu Pro Val Ser Glu Thr Cys Asp Thr Tyr Ser Tyr Gly Val Val
180                 185                 190                 195

ctc tgg gag atg cta aca agg gag gtc ccc ttt aaa ggt ttg gaa gga   679
Leu Trp Glu Met Leu Thr Arg Glu Val Pro Phe Lys Gly Leu Glu Gly
                200                 205                 210

tta caa gta gct tgg ctt gta gtg gaa aaa aac gag aga tta acc att   727
Leu Gln Val Ala Trp Leu Val Val Glu Lys Asn Glu Arg Leu Thr Ile
            215                 220                 225

cca agc agt tgc ccc aga agt ttt gct gaa ctg tta cat cag tgt tgg   775
Pro Ser Ser Cys Pro Arg Ser Phe Ala Glu Leu Leu His Gln Cys Trp
        230                 235                 240

gaa gct gat gcc aag aaa cgg cca tca ttc aag caa atc att tca atc   823
Glu Ala Asp Ala Lys Lys Arg Pro Ser Phe Lys Gln Ile Ile Ser Ile
    245                 250                 255

ctg gag tcc atg tca aat gac acg agc ctt cct gac aag tgt aac tca   871
Leu Glu Ser Met Ser Asn Asp Thr Ser Leu Pro Asp Lys Cys Asn Ser
260                 265                 270                 275

ttc cta cac aac aag gcg gag tgg agg tgc gaa att gag gca act ctt   919
Phe Leu His Asn Lys Ala Glu Trp Arg Cys Glu Ile Glu Ala Thr Leu
                280                 285                 290

gag agg cta aag aaa cta gag cgt gat ctc agc ttt aag gag cag gag   967
Glu Arg Leu Lys Lys Leu Glu Arg Asp Leu Ser Phe Lys Glu Gln Glu
            295                 300                 305
```

```
ctt aaa gaa cga gaa aga cgt tta aag atg tgg gag caa aag ctg aca   1015
Leu Lys Glu Arg Glu Arg Arg Leu Lys Met Trp Glu Gln Lys Leu Thr
        310                 315                 320

gag cag tcc aac acc ccg ctt ctc ttg cct ctt gct gca aga atg tct   1063
Glu Gln Ser Asn Thr Pro Leu Leu Leu Pro Leu Ala Ala Arg Met Ser
    325                 330                 335

gag gag tct tac ttt gaa tct aaa aca gag gag tca aac agt gca gag   1111
Glu Glu Ser Tyr Phe Glu Ser Lys Thr Glu Glu Ser Asn Ser Ala Glu
340                 345                 350                 355

atg tca tgt cag atc aca gca aca agt aac ggg gag ggc cat ggc atg   1159
Met Ser Cys Gln Ile Thr Ala Thr Ser Asn Gly Glu Gly His Gly Met
                360                 365                 370

aac cca agt ctg cag gcc atg atg ctg atg ggc ttt ggg gat atc ttc   1207
Asn Pro Ser Leu Gln Ala Met Met Leu Met Gly Phe Gly Asp Ile Phe
            375                 380                 385

tca atg aac aaa gca gga gct gtg atg cat tct ggg atg cag ata aac   1255
Ser Met Asn Lys Ala Gly Ala Val Met His Ser Gly Met Gln Ile Asn
        390                 395                 400

atg caa gcc aag cag aat tct tcc aaa acc aca tct aag aga agg ggg   1303
Met Gln Ala Lys Gln Asn Ser Ser Lys Thr Thr Ser Lys Arg Arg Gly
    405                 410                 415

aag aaa gtc aac atg gct ctg ggg ttc agt gat ttt gac ttg tca gaa   1351
Lys Lys Val Asn Met Ala Leu Gly Phe Ser Asp Phe Asp Leu Ser Glu
420                 425                 430                 435

ggt gac gat gat gat gat gat gac ggt gag gag gag gat aat gac atg   1399
Gly Asp Asp Asp Asp Asp Asp Asp Gly Glu Glu Glu Asp Asn Asp Met
                440                 445                 450

gat aat agt gaa tgaaagcaga aagcaaagta ataaaatcac aaatgtttgg       1451
Asp Asn Ser Glu
            455

aaaacacaaa agtaacttgt ttatctcagt ctgtacaaaa acagtaagga ggcagaaagc 1511

caagcactgc atttttaggc caatcacatt tacatgaccg taatttctta tcaattctac 1571

ttttatttt gcttacagaa aaacgggggg agaattaagc caaagaagta tatttatgaa 1631

tcagcaaatg tggtgcctga ttatagaaat ttgtgatcct atatacaata taggactttt 1691

aaagttgtga cattctggct ttttctttta atgaatactt tttagtttgt atttgacttt 1751

atttccttta ttcaaatcat ttttaaaaac ttacattttg aacaaacact cttaactcct 1811

aattgttctt tgacacgtag taattctgtg acatactttt ttttttcttat agcaatacac 1871

tgtaatatca gaaatggttg gcctgagcaa cctagtaaga cctcgtctct actaataatt 1931

aaaaaactag ctggcatggt agcacacacc tgtagtccca gatacttggg aggccaaggc 1991
```

aggaggattg cttgagacct agcaatcagt cagggctgca gtgagccatg atggcaccac 2051

tgcactctag cctgggcaag agaacaagat cctgtctcaa aaaacaaaaa aaaaaaaaaa 2111

gggcggccg 2120

<210> 5
<211> 455
<212> PRT
<213> Homo sapiens

<400> 5

```
Met Ser Ser Leu Gly Ala Ser Phe Val Gln Ile Lys Phe Asp Asp Leu
  1               5                  10                  15

Gln Phe Phe Glu Asn Cys Gly Gly Gly Ser Phe Gly Ser Val Tyr Arg
             20                  25                  30

Ala Lys Trp Ile Ser Gln Asp Lys Glu Val Ala Val Lys Lys Leu Leu
         35                  40                  45

Lys Ile Glu Lys Glu Ala Glu Ile Leu Ser Val Leu Ser His Arg Asn
     50                  55                  60

Ile Ile Gln Phe Tyr Gly Val Ile Leu Glu Pro Pro Asn Tyr Gly Ile
 65                  70                  75                  80

Val Thr Glu Tyr Ala Ser Leu Gly Ser Leu Tyr Asp Tyr Ile Asn Ser
                 85                  90                  95

Asn Arg Ser Glu Glu Met Asp Met Asp His Ile Met Thr Trp Ala Thr
            100                 105                 110

Asp Val Ala Lys Gly Met His Tyr Leu His Met Glu Ala Pro Val Lys
        115                 120                 125

Val Ile His Arg Asp Leu Lys Ser Arg Asn Val Val Ile Ala Ala Asp
    130                 135                 140

Gly Val Leu Lys Ile Cys Asp Phe Gly Ala Ser Arg Phe His Asn His
145                 150                 155                 160

Thr Thr His Met Ser Leu Val Gly Thr Phe Pro Trp Met Ala Pro Glu
                165                 170                 175

Val Ile Gln Ser Leu Pro Val Ser Glu Thr Cys Asp Thr Tyr Ser Tyr
            180                 185                 190

Gly Val Val Leu Trp Glu Met Leu Thr Arg Glu Val Pro Phe Lys Gly
        195                 200                 205

Leu Glu Gly Leu Gln Val Ala Trp Leu Val Val Glu Lys Asn Glu Arg
    210                 215                 220

Leu Thr Ile Pro Ser Ser Cys Pro Arg Ser Phe Ala Glu Leu Leu His
```

225 230 235 240

Gln Cys Trp Glu Ala Asp Ala Lys Lys Arg Pro Ser Phe Lys Gln Ile
245 250 255

Ile Ser Ile Leu Glu Ser Met Ser Asn Asp Thr Ser Leu Pro Asp Lys
260 265 270

Cys Asn Ser Phe Leu His Asn Lys Ala Glu Trp Arg Cys Glu Ile Glu
275 280 285

Ala Thr Leu Glu Arg Leu Lys Lys Leu Glu Arg Asp Leu Ser Phe Lys
290 295 300

Glu Gln Glu Leu Lys Glu Arg Glu Arg Arg Leu Lys Met Trp Glu Gln
305 310 315 320

Lys Leu Thr Glu Gln Ser Asn Thr Pro Leu Leu Leu Pro Leu Ala Ala
325 330 335

Arg Met Ser Glu Glu Ser Tyr Phe Glu Ser Lys Thr Glu Glu Ser Asn
340 345 350

Ser Ala Glu Met Ser Cys Gln Ile Thr Ala Thr Ser Asn Gly Glu Gly
355 360 365

His Gly Met Asn Pro Ser Leu Gln Ala Met Met Leu Met Gly Phe Gly
370 375 380

Asp Ile Phe Ser Met Asn Lys Ala Gly Ala Val Met His Ser Gly Met
385 390 395 400

Gln Ile Asn Met Gln Ala Lys Gln Asn Ser Ser Lys Thr Thr Ser Lys
405 410 415

Arg Arg Gly Lys Lys Val Asn Met Ala Leu Gly Phe Ser Asp Phe Asp
420 425 430

Leu Ser Glu Gly Asp Asp Asp Asp Asp Asp Asp Gly Glu Glu Glu Asp
435 440 445

Asn Asp Met Asp Asn Ser Glu
450 455

<210> 6
<211> 1365
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1365)

<400> 6
atg tcg tct ctc ggt gcc tcc ttt gtg caa att aaa ttt gat gac ttg 48
Met Ser Ser Leu Gly Ala Ser Phe Val Gln Ile Lys Phe Asp Asp Leu

```
1               5                  10                  15

cag ttt ttt gaa aac tgc ggt gga gga agt ttt ggg agt gtt tat cga   96
Gln Phe Phe Glu Asn Cys Gly Gly Gly Ser Phe Gly Ser Val Tyr Arg
            20                  25                  30

gcc aaa tgg ata tca cag gac aag gag gtg gct gta aag aag ctc ctc   144
Ala Lys Trp Ile Ser Gln Asp Lys Glu Val Ala Val Lys Lys Leu Leu
        35                  40                  45

aaa ata gag aaa gag gca gaa ata ctc agt gtc ctc agt cac aga aac   192
Lys Ile Glu Lys Glu Ala Glu Ile Leu Ser Val Leu Ser His Arg Asn
    50                  55                  60

atc atc cag ttt tat gga gta att ctt gaa cct ccc aac tat ggc att   240
Ile Ile Gln Phe Tyr Gly Val Ile Leu Glu Pro Pro Asn Tyr Gly Ile
65                  70                  75                  80

gtc aca gaa tat gct tct ctg gga tca ctc tat gat tac att aac agt   288
Val Thr Glu Tyr Ala Ser Leu Gly Ser Leu Tyr Asp Tyr Ile Asn Ser
                85                  90                  95

aac aga agt gag gag atg gat atg gat cac att atg acc tgg gcc act   336
Asn Arg Ser Glu Glu Met Asp Met Asp His Ile Met Thr Trp Ala Thr
            100                 105                 110

gat gta gcc aaa gga atg cat tat tta cat atg gag gct cct gtc aag   384
Asp Val Ala Lys Gly Met His Tyr Leu His Met Glu Ala Pro Val Lys
        115                 120                 125

gtg att cac aga gac ctc aag tca aga aac gtt gtt ata gct gct gat   432
Val Ile His Arg Asp Leu Lys Ser Arg Asn Val Val Ile Ala Ala Asp
    130                 135                 140

gga gta ctg aag atc tgt gac ttt ggt gcc tct cgg ttc cat aac cat   480
Gly Val Leu Lys Ile Cys Asp Phe Gly Ala Ser Arg Phe His Asn His
145                 150                 155                 160

aca aca cac atg tcc ttg gtt gga act ttc cca tgg atg gct cca gaa   528
Thr Thr His Met Ser Leu Val Gly Thr Phe Pro Trp Met Ala Pro Glu
                165                 170                 175

gtt atc cag agt ctc cct gtg tca gaa act tgt gac aca tat tcc tat   576
Val Ile Gln Ser Leu Pro Val Ser Glu Thr Cys Asp Thr Tyr Ser Tyr
            180                 185                 190

ggt gtg gtt ctc tgg gag atg cta aca agg gag gtc ccc ttt aaa ggt   624
Gly Val Val Leu Trp Glu Met Leu Thr Arg Glu Val Pro Phe Lys Gly
        195                 200                 205

ttg gaa gga tta caa gta gct tgg ctt gta gtg gaa aaa aac gag aga   672
Leu Glu Gly Leu Gln Val Ala Trp Leu Val Val Glu Lys Asn Glu Arg
    210                 215                 220

tta acc att cca agc agt tgc ccc aga agt ttt gct gaa ctg tta cat   720
Leu Thr Ile Pro Ser Ser Cys Pro Arg Ser Phe Ala Glu Leu Leu His
225                 230                 235                 240
```

```
cag tgt tgg gaa gct gat gcc aag aaa cgg cca tca ttc aag caa atc   768
Gln Cys Trp Glu Ala Asp Ala Lys Lys Arg Pro Ser Phe Lys Gln Ile
                245                 250                 255

att tca atc ctg gag tcc atg tca aat gac acg agc ctt cct gac aag   816
Ile Ser Ile Leu Glu Ser Met Ser Asn Asp Thr Ser Leu Pro Asp Lys
            260                 265                 270

tgt aac tca ttc cta cac aac aag gcg gag tgg agg tgc gaa att gag   864
Cys Asn Ser Phe Leu His Asn Lys Ala Glu Trp Arg Cys Glu Ile Glu
        275                 280                 285

gca act ctt gag agg cta aag aaa cta gag cgt gat ctc agc ttt aag   912
Ala Thr Leu Glu Arg Leu Lys Lys Leu Glu Arg Asp Leu Ser Phe Lys
    290                 295                 300

gag cag gag ctt aaa gaa cga gaa aga cgt tta aag atg tgg gag caa   960
Glu Gln Glu Leu Lys Glu Arg Glu Arg Arg Leu Lys Met Trp Glu Gln
305                 310                 315                 320

aag ctg aca gag cag tcc aac acc ccg ctt ctc ttg cct ctt gct gca  1008
Lys Leu Thr Glu Gln Ser Asn Thr Pro Leu Leu Leu Pro Leu Ala Ala
                325                 330                 335

aga atg tct gag gag tct tac ttt gaa tct aaa aca gag gag tca aac  1056
Arg Met Ser Glu Glu Ser Tyr Phe Glu Ser Lys Thr Glu Glu Ser Asn
            340                 345                 350

agt gca gag atg tca tgt cag atc aca gca aca agt aac ggg gag ggc  1104
Ser Ala Glu Met Ser Cys Gln Ile Thr Ala Thr Ser Asn Gly Glu Gly
        355                 360                 365

cat ggc atg aac cca agt ctg cag gcc atg atg ctg atg ggc ttt ggg  1152
His Gly Met Asn Pro Ser Leu Gln Ala Met Met Leu Met Gly Phe Gly
    370                 375                 380

gat atc ttc tca atg aac aaa gca gga gct gtg atg cat tct ggg atg  1200
Asp Ile Phe Ser Met Asn Lys Ala Gly Ala Val Met His Ser Gly Met
385                 390                 395                 400

cag ata aac atg caa gcc aag cag aat tct tcc aaa acc aca tct aag  1248
Gln Ile Asn Met Gln Ala Lys Gln Asn Ser Ser Lys Thr Thr Ser Lys
                405                 410                 415

aga agg ggg aag aaa gtc aac atg gct ctg ggg ttc agt gat ttt gac  1296
Arg Arg Gly Lys Lys Val Asn Met Ala Leu Gly Phe Ser Asp Phe Asp
            420                 425                 430

ttg tca gaa ggt gac gat gat gat gat gat gac ggt gag gag gag gat  1344
Leu Ser Glu Gly Asp Asp Asp Asp Asp Asp Asp Gly Glu Glu Glu Asp
        435                 440                 445

aat gac atg gat aat agt gaa                                     1365
Asn Asp Met Asp Asn Ser Glu
    450                 455
```

<210> 7
<211> 2454
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (51)..(1793)

<400> 7

```
cggtggtggc ggcagcggcg gctgcggggg caccgggccg cggcgccacc atg gcg    56
                                                        Met Ala
                                                          1

gtg cga cag gcg ctg ggc cgc ggc ctg cag ctg ggt cga gcg ctg ctg   104
Val Arg Gln Ala Leu Gly Arg Gly Leu Gln Leu Gly Arg Ala Leu Leu
          5                  10                  15

ctg cgc ttc acg ggc aag ccc ggc cgg gcc tac ggc ttg ggg cgg ccg   152
Leu Arg Phe Thr Gly Lys Pro Gly Arg Ala Tyr Gly Leu Gly Arg Pro
     20                  25                  30

ggc ccg gcg gcg ggc tgt gtc cgc ggg gag cgt cca ggc tgg gcc gca   200
Gly Pro Ala Ala Gly Cys Val Arg Gly Glu Arg Pro Gly Trp Ala Ala
 35                  40                  45                  50

gga ccg ggc gcg gag cct cgc agg gtc ggg ctc ggg ctt cct aac cgt   248
Gly Pro Gly Ala Glu Pro Arg Arg Val Gly Leu Gly Leu Pro Asn Arg
                 55                  60                  65

ctc cgc ttc ttc cgc cag tcg gtg gcc ggg ctg gcg gcg cgg ttg cag   296
Leu Arg Phe Phe Arg Gln Ser Val Ala Gly Leu Ala Ala Arg Leu Gln
             70                  75                  80

cgg cag ttc gtg gtg cgg gcc tgg ggc tgc gcg ggc cct tgc ggc cgg   344
Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys Gly Arg
         85                  90                  95

gca gtc ttt ctg gcc ttc ggg cta ggg ctg ggc ctc atc gag gaa aaa   392
Ala Val Phe Leu Ala Phe Gly Leu Gly Leu Gly Leu Ile Glu Glu Lys
    100                 105                 110

cag gcg gag agc cgg cgg gcg gtc tcg gcc tgt cag gag atc cag gca   440
Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile Gln Ala
115                 120                 125                 130

att ttt acc cag aaa agc aag ccg ggg cct gac ccg ttg gac acg aga   488
Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp Thr Arg
                135                 140                 145

cgc ttg cag ggc ttt cgg ctg gag gag tat ctg ata ggg cag tcc att   536
Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln Ser Ile
            150                 155                 160

ggt aag ggc tgc agt gct gct gtg tat gaa gcc acc atg cct aca ttg   584
Gly Lys Gly Cys Ser Ala Ala Val Tyr Glu Ala Thr Met Pro Thr Leu
```

```
        165                 170                 175

ccc cag aac ctg gag gtg aca aag agc acc ggg ttg ctt cca ggg aga   632
Pro Gln Asn Leu Glu Val Thr Lys Ser Thr Gly Leu Leu Pro Gly Arg
    180                 185                 190

ggc cca ggt acc agt gca cca gga gaa ggg cag gag cga gct ccg ggg   680
Gly Pro Gly Thr Ser Ala Pro Gly Glu Gly Gln Glu Arg Ala Pro Gly
195                 200                 205                 210

gcc cct gcc ttc ccc ttg gcc atc aag atg atg tgg aac atc tcg gca   728
Ala Pro Ala Phe Pro Leu Ala Ile Lys Met Met Trp Asn Ile Ser Ala
                215                 220                 225

ggt tcc tcc agc gaa gcc atc ttg aac aca atg agc cag gag ctg gtc   776
Gly Ser Ser Ser Glu Ala Ile Leu Asn Thr Met Ser Gln Glu Leu Val
            230                 235                 240

cca gcg agc cga gtg gcc ttg gct ggg gag tat gga gca gtc act tac   824
Pro Ala Ser Arg Val Ala Leu Ala Gly Glu Tyr Gly Ala Val Thr Tyr
        245                 250                 255

aga aaa tcc aag aga ggt ccc aag caa cta gcc cct cac ccc aac atc   872
Arg Lys Ser Lys Arg Gly Pro Lys Gln Leu Ala Pro His Pro Asn Ile
    260                 265                 270

atc cgg gtt ctc cgc gcc ttc acc tct tcc gtg ccg ctg ctg cca ggg   920
Ile Arg Val Leu Arg Ala Phe Thr Ser Ser Val Pro Leu Leu Pro Gly
275                 280                 285                 290

gcc ctg gtc gac tac cct gat gtg ctg ccc tca cgc ctc cac cct gaa   968
Ala Leu Val Asp Tyr Pro Asp Val Leu Pro Ser Arg Leu His Pro Glu
                295                 300                 305

ggc ctg ggc cat ggc cgg acg ctg ttc ctc gtt atg aag aac tat ccc   1016
Gly Leu Gly His Gly Arg Thr Leu Phe Leu Val Met Lys Asn Tyr Pro
            310                 315                 320

tgt acc ctg cgc cag tac ctt tgt gtg aac aca ccc agc ccc cgc ctc   1064
Cys Thr Leu Arg Gln Tyr Leu Cys Val Asn Thr Pro Ser Pro Arg Leu
        325                 330                 335

gcc gcc atg atg ctg ctg cag ctg ctg gaa ggc gtg gac cat ctg gtt   1112
Ala Ala Met Met Leu Leu Gln Leu Leu Glu Gly Val Asp His Leu Val
    340                 345                 350

caa cag ggc atc gcg cac aga gac ctg aaa tcc gac aac atc ctt gtg   1160
Gln Gln Gly Ile Ala His Arg Asp Leu Lys Ser Asp Asn Ile Leu Val
355                 360                 365                 370

gag ctg gac cca gac ggc tgc ccc tgg ctg gtg atc gca gat ttt ggc   1208
Glu Leu Asp Pro Asp Gly Cys Pro Trp Leu Val Ile Ala Asp Phe Gly
                375                 380                 385

tgc tgc ctg gct gat gag agc atc ggc ctg cag ttg ccc ttc agc agc   1256
Cys Cys Leu Ala Asp Glu Ser Ile Gly Leu Gln Leu Pro Phe Ser Ser
            390                 395                 400
```

```
tgg tac gtg gat cgg ggc gga aac ggc tgt ctg atg gcc cca gag gtg   1304
Trp Tyr Val Asp Arg Gly Gly Asn Gly Cys Leu Met Ala Pro Glu Val
        405                 410                 415

tcc acg gcc cgt cct ggc ccc agg gca gtg att gac tac agc aag gct   1352
Ser Thr Ala Arg Pro Gly Pro Arg Ala Val Ile Asp Tyr Ser Lys Ala
    420                 425                 430

gat gcc tgg gca gtg gga gcc atc gcc tat gaa atc ttc ggg ctt gtc   1400
Asp Ala Trp Ala Val Gly Ala Ile Ala Tyr Glu Ile Phe Gly Leu Val
435                 440                 445                 450

aat ccc ttc tac ggc cag ggc aag gcc cac ctt gaa agc cgc agc tac   1448
Asn Pro Phe Tyr Gly Gln Gly Lys Ala His Leu Glu Ser Arg Ser Tyr
                455                 460                 465

caa gag gct cag cta cct gca ctg ccc gag tca gtg cct cca gac gtg   1496
Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro Asp Val
            470                 475                 480

aga cag ttg gtg agg gca ctg ctc cag cga gag gcc agc aag aga cca   1544
Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys Arg Pro
        485                 490                 495

tct gcc cga gta gcc gca aat gtg ctt cat cta agc ctc tgg ggt gaa   1592
Ser Ala Arg Val Ala Ala Asn Val Leu His Leu Ser Leu Trp Gly Glu
    500                 505                 510

cat att cta gcc ctg aag aat ctg aag tta gac aag atg gtt ggc tgg   1640
His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val Gly Trp
515                 520                 525                 530

ctc ctc caa caa tcg gcc gcc act ttg ttg gcc aac agg ctc aca gag   1688
Leu Leu Gln Gln Ser Ala Ala Thr Leu Leu Ala Asn Arg Leu Thr Glu
                535                 540                 545

aag tgt tgt gtg gaa aca aaa atg aag atg ctc ttt ctg gct aac ctg   1736
Lys Cys Cys Val Glu Thr Lys Met Lys Met Leu Phe Leu Ala Asn Leu
            550                 555                 560

gag tgt gaa acg ctc tgc cag gca gcc ctc ctc ctc tgc tca tgg agg   1784
Glu Cys Glu Thr Leu Cys Gln Ala Ala Leu Leu Leu Cys Ser Trp Arg
        565                 570                 575

gca gcc ctg tgatgtccct gcatggagct ggtgaattac taaaagaact           1833
Ala Ala Leu
    580

tggcatcctc tgtgtcgtga tggtctgtga atggtgaggg tgggagtcag gagacaagac 1893

agcgcagaga gggctggtta gccggaaaag gcctcgggct tggcaaatgg aagaacttga 1953

gtgagagttc agtctgcagt cctctgctca cagacatctg aaaagtgaat ggccaagctg 2013

gtctagtaga tgaggctgga ctgaggaggg gtaggcctgc atccacagag aggatccagg 2073
```

ccaaggcact ggctgtcagt ggcagagttt ggctgtgacc tttgccccta acacgaggaa 2133

ctcgtttgaa gggggcagcg tagcatgtct gatttgccac ctggatgaag gcagacatca 2193

acatgggtca gcacgttcag ttacgggagt gggaaattac atgaggcctg ggcctctgcg 2253

ttcccaagct gtgcgttctg gaccagctac tgaattatta atctcactta gcgaaagtga 2313

cggatgagca gtaagtaagt aagtgtgggg atttaaactt gagggtttcc ctcctgacta 2373

gcctctctta caggaattgt gaaatattaa atgcaaattt acaactgcaa aaaaaaaaaa 2433

aaaaaaaaaa aagggcggcc c 2454

<210> 8
<211> 581
<212> PRT
<213> Homo sapiens

<400> 8

```
Met Ala Val Arg Gln Ala Leu Gly Arg Gly Leu Gln Leu Gly Arg Ala
  1               5                  10                  15

Leu Leu Leu Arg Phe Thr Gly Lys Pro Gly Arg Ala Tyr Gly Leu Gly
             20                  25                  30

Arg Pro Gly Pro Ala Ala Gly Cys Val Arg Gly Glu Arg Pro Gly Trp
         35                  40                  45

Ala Ala Gly Pro Gly Ala Glu Pro Arg Arg Val Gly Leu Gly Leu Pro
     50                  55                  60

Asn Arg Leu Arg Phe Phe Arg Gln Ser Val Ala Gly Leu Ala Ala Arg
 65                  70                  75                  80

Leu Gln Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys
                 85                  90                  95

Gly Arg Ala Val Phe Leu Ala Phe Gly Leu Gly Leu Gly Leu Ile Glu
            100                 105                 110

Glu Lys Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile
        115                 120                 125

Gln Ala Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp
    130                 135                 140

Thr Arg Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln
145                 150                 155                 160

Ser Ile Gly Lys Gly Cys Ser Ala Ala Val Tyr Glu Ala Thr Met Pro
                165                 170                 175

Thr Leu Pro Gln Asn Leu Glu Val Thr Lys Ser Thr Gly Leu Leu Pro
            180                 185                 190
```

Gly Arg Gly Pro Gly Thr Ser Ala Pro Gly Glu Gly Gln Glu Arg Ala
195 200 205

Pro Gly Ala Pro Ala Phe Pro Leu Ala Ile Lys Met Met Trp Asn Ile
210 215 220

Ser Ala Gly Ser Ser Ser Glu Ala Ile Leu Asn Thr Met Ser Gln Glu
225 230 235 240

Leu Val Pro Ala Ser Arg Val Ala Leu Ala Gly Glu Tyr Gly Ala Val
245 250 255

Thr Tyr Arg Lys Ser Lys Arg Gly Pro Lys Gln Leu Ala Pro His Pro
260 265 270

Asn Ile Ile Arg Val Leu Arg Ala Phe Thr Ser Ser Val Pro Leu Leu
275 280 285

Pro Gly Ala Leu Val Asp Tyr Pro Asp Val Leu Pro Ser Arg Leu His
290 295 300

Pro Glu Gly Leu Gly His Gly Arg Thr Leu Phe Leu Val Met Lys Asn
305 310 315 320

Tyr Pro Cys Thr Leu Arg Gln Tyr Leu Cys Val Asn Thr Pro Ser Pro
325 330 335

Arg Leu Ala Ala Met Met Leu Leu Gln Leu Leu Glu Gly Val Asp His
340 345 350

Leu Val Gln Gln Gly Ile Ala His Arg Asp Leu Lys Ser Asp Asn Ile
355 360 365

Leu Val Glu Leu Asp Pro Asp Gly Cys Pro Trp Leu Val Ile Ala Asp
370 375 380

Phe Gly Cys Cys Leu Ala Asp Glu Ser Ile Gly Leu Gln Leu Pro Phe
385 390 395 400

Ser Ser Trp Tyr Val Asp Arg Gly Gly Asn Gly Cys Leu Met Ala Pro
405 410 415

Glu Val Ser Thr Ala Arg Pro Gly Pro Arg Ala Val Ile Asp Tyr Ser
420 425 430

Lys Ala Asp Ala Trp Ala Val Gly Ala Ile Ala Tyr Glu Ile Phe Gly
435 440 445

Leu Val Asn Pro Phe Tyr Gly Gln Gly Lys Ala His Leu Glu Ser Arg
450 455 460

Ser Tyr Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro
465 470 475 480

Asp Val Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys
485 490 495

```
Arg Pro Ser Ala Arg Val Ala Ala Asn Val Leu His Leu Ser Leu Trp
            500                 505                 510

Gly Glu His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val
        515                 520                 525

Gly Trp Leu Leu Gln Gln Ser Ala Ala Thr Leu Leu Ala Asn Arg Leu
    530                 535                 540

Thr Glu Lys Cys Cys Val Glu Thr Lys Met Lys Met Leu Phe Leu Ala
545                 550                 555                 560

Asn Leu Glu Cys Glu Thr Leu Cys Gln Ala Ala Leu Leu Leu Cys Ser
                565                 570                 575

Trp Arg Ala Ala Leu
            580
```

<210> 9
<211> 1743
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1743)

<400> 9

```
atg gcg gtg cga cag gcg ctg ggc cgc ggc ctg cag ctg ggt cga gcg   48
Met Ala Val Arg Gln Ala Leu Gly Arg Gly Leu Gln Leu Gly Arg Ala
  1               5                  10                  15

ctg ctg ctg cgc ttc acg ggc aag ccc ggc cgg gcc tac ggc ttg ggg   96
Leu Leu Leu Arg Phe Thr Gly Lys Pro Gly Arg Ala Tyr Gly Leu Gly
             20                  25                  30

cgg ccg ggc ccg gcg gcg ggc tgt gtc cgc ggg gag cgt cca ggc tgg   144
Arg Pro Gly Pro Ala Ala Gly Cys Val Arg Gly Glu Arg Pro Gly Trp
         35                  40                  45

gcc gca gga ccg ggc gcg gag cct cgc agg gtc ggg ctc ggg ctt cct   192
Ala Ala Gly Pro Gly Ala Glu Pro Arg Arg Val Gly Leu Gly Leu Pro
     50                  55                  60

aac cgt ctc cgc ttc ttc cgc cag tcg gtg gcc ggg ctg gcg gcg cgg   240
Asn Arg Leu Arg Phe Phe Arg Gln Ser Val Ala Gly Leu Ala Ala Arg
 65                  70                  75                  80

ttg cag cgg cag ttc gtg gtg cgg gcc tgg ggc tgc gcg ggc cct tgc   288
Leu Gln Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys
                 85                  90                  95

ggc cgg gca gtc ttt ctg gcc ttc ggg cta ggg ctg ggc ctc atc gag   336
Gly Arg Ala Val Phe Leu Ala Phe Gly Leu Gly Leu Gly Leu Ile Glu
            100                 105                 110
```

```
gaa aaa cag gcg gag agc cgg cgg gcg gtc tcg gcc tgt cag gag atc   384
Glu Lys Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile
        115                 120                 125

cag gca att ttt acc cag aaa agc aag ccg ggg cct gac ccg ttg gac   432
Gln Ala Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp
    130                 135                 140

acg aga cgc ttg cag ggc ttt cgg ctg gag gag tat ctg ata ggg cag   480
Thr Arg Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln
145                 150                 155                 160

tcc att ggt aag ggc tgc agt gct gct gtg tat gaa gcc acc atg cct   528
Ser Ile Gly Lys Gly Cys Ser Ala Ala Val Tyr Glu Ala Thr Met Pro
                165                 170                 175

aca ttg ccc cag aac ctg gag gtg aca aag agc acc ggg ttg ctt cca   576
Thr Leu Pro Gln Asn Leu Glu Val Thr Lys Ser Thr Gly Leu Leu Pro
            180                 185                 190

ggg aga ggc cca ggt acc agt gca cca gga gaa ggg cag gag cga gct   624
Gly Arg Gly Pro Gly Thr Ser Ala Pro Gly Glu Gly Gln Glu Arg Ala
        195                 200                 205

ccg ggg gcc cct gcc ttc ccc ttg gcc atc aag atg atg tgg aac atc   672
Pro Gly Ala Pro Ala Phe Pro Leu Ala Ile Lys Met Met Trp Asn Ile
    210                 215                 220

tcg gca ggt tcc tcc agc gaa gcc atc ttg aac aca atg agc cag gag   720
Ser Ala Gly Ser Ser Ser Glu Ala Ile Leu Asn Thr Met Ser Gln Glu
225                 230                 235                 240

ctg gtc cca gcg agc cga gtg gcc ttg gct ggg gag tat gga gca gtc   768
Leu Val Pro Ala Ser Arg Val Ala Leu Ala Gly Glu Tyr Gly Ala Val
                245                 250                 255

act tac aga aaa tcc aag aga ggt ccc aag caa cta gcc cct cac ccc   816
Thr Tyr Arg Lys Ser Lys Arg Gly Pro Lys Gln Leu Ala Pro His Pro
            260                 265                 270

aac atc atc cgg gtt ctc cgc gcc ttc acc tct tcc gtg ccg ctg ctg   864
Asn Ile Ile Arg Val Leu Arg Ala Phe Thr Ser Ser Val Pro Leu Leu
        275                 280                 285

cca ggg gcc ctg gtc gac tac cct gat gtg ctg ccc tca cgc ctc cac   912
Pro Gly Ala Leu Val Asp Tyr Pro Asp Val Leu Pro Ser Arg Leu His
    290                 295                 300

cct gaa ggc ctg ggc cat ggc cgg acg ctg ttc ctc gtt atg aag aac   960
Pro Glu Gly Leu Gly His Gly Arg Thr Leu Phe Leu Val Met Lys Asn
305                 310                 315                 320

tat ccc tgt acc ctg cgc cag tac ctt tgt gtg aac aca ccc agc ccc  1008
Tyr Pro Cys Thr Leu Arg Gln Tyr Leu Cys Val Asn Thr Pro Ser Pro
                325                 330                 335

cgc ctc gcc gcc atg atg ctg ctg cag ctg ctg gaa ggc gtg gac cat  1056
```

```
Arg Leu Ala Ala Met Met Leu Leu Gln Leu Leu Glu Gly Val Asp His
            340                 345                 350

ctg gtt caa cag ggc atc gcg cac aga gac ctg aaa tcc gac aac atc   1104
Leu Val Gln Gln Gly Ile Ala His Arg Asp Leu Lys Ser Asp Asn Ile
        355                 360                 365

ctt gtg gag ctg gac cca gac ggc tgc ccc tgg ctg gtg atc gca gat   1152
Leu Val Glu Leu Asp Pro Asp Gly Cys Pro Trp Leu Val Ile Ala Asp
    370                 375                 380

ttt ggc tgc tgc ctg gct gat gag agc atc ggc ctg cag ttg ccc ttc   1200
Phe Gly Cys Cys Leu Ala Asp Glu Ser Ile Gly Leu Gln Leu Pro Phe
385                 390                 395                 400

agc agc tgg tac gtg gat cgg ggc gga aac ggc tgt ctg atg gcc cca   1248
Ser Ser Trp Tyr Val Asp Arg Gly Gly Asn Gly Cys Leu Met Ala Pro
                405                 410                 415

gag gtg tcc acg gcc cgt cct ggc ccc agg gca gtg att gac tac agc   1296
Glu Val Ser Thr Ala Arg Pro Gly Pro Arg Ala Val Ile Asp Tyr Ser
            420                 425                 430

aag gct gat gcc tgg gca gtg gga gcc atc gcc tat gaa atc ttc ggg   1344
Lys Ala Asp Ala Trp Ala Val Gly Ala Ile Ala Tyr Glu Ile Phe Gly
        435                 440                 445

ctt gtc aat ccc ttc tac ggc cag ggc aag gcc cac ctt gaa agc cgc   1392
Leu Val Asn Pro Phe Tyr Gly Gln Gly Lys Ala His Leu Glu Ser Arg
    450                 455                 460

agc tac caa gag gct cag cta cct gca ctg ccc gag tca gtg cct cca   1440
Ser Tyr Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro
465                 470                 475                 480

gac gtg aga cag ttg gtg agg gca ctg ctc cag cga gag gcc agc aag   1488
Asp Val Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys
                485                 490                 495

aga cca tct gcc cga gta gcc gca aat gtg ctt cat cta agc ctc tgg   1536
Arg Pro Ser Ala Arg Val Ala Ala Asn Val Leu His Leu Ser Leu Trp
            500                 505                 510

ggt gaa cat att cta gcc ctg aag aat ctg aag tta gac aag atg gtt   1584
Gly Glu His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val
        515                 520                 525

ggc tgg ctc ctc caa caa tcg gcc gcc act ttg ttg gcc aac agg ctc   1632
Gly Trp Leu Leu Gln Gln Ser Ala Ala Thr Leu Leu Ala Asn Arg Leu
    530                 535                 540

aca gag aag tgt tgt gtg gaa aca aaa atg aag atg ctc ttt ctg gct   1680
Thr Glu Lys Cys Cys Val Glu Thr Lys Met Lys Met Leu Phe Leu Ala
545                 550                 555                 560

aac ctg gag tgt gaa acg ctc tgc cag gca gcc ctc ctc ctc tgc tca   1728
Asn Leu Glu Cys Glu Thr Leu Cys Gln Ala Ala Leu Leu Leu Cys Ser
```

```
                565                 570                 575

tgg agg gca gcc ctg                                                 1743
Trp Arg Ala Ala Leu
            580
```

<210> 10
<211> 1864
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (275)..(754)

<400> 10

```
gtcgacccac gcggtccgcc cacgcgttcc ggagacatgt ctctgtgttt ctctcccctc 60

cgcttttgag tccgttgaag acacaatttc tctctgtcgg gtgcttagga ggagctccat 120

gaacatgtat tgaattggac ttagctgaac aggctgctgg ttggctgccc agaggggca 180

ggctgtgttg ctgggagcct tccagctccc tgcagcagtc atggggcagg gttccccgag 240

tccgtaatcc ccatttccac ctactttccc ttag tta ttt gat tcc ctg tct gtc 295
                                     Leu Phe Asp Ser Leu Ser Val
                                       1               5

gta ctc agc tta agt gga gca tcc cct ttc ctg gga gac acg aag cag   343
Val Leu Ser Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln
         10                  15                  20

gaa aca ctg gca aat atc aca gca gtg agt tac gac ttt gat gag gaa   391
Glu Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu
     25                  30                  35

ttc ttc agc cag acg agc gag ctg gcc aag gac ttt att cgg aag ctt   439
Phe Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu
 40                  45                  50                  55

ctg gtt aaa gag acc cgg aaa cgg ctc aca atc caa gag gct ctc aga   487
Leu Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg
                 60                  65                  70

cac ccc tgg atc acg ccg gtg gac aac cag caa gcc atg gtg cgc agg   535
His Pro Trp Ile Thr Pro Val Asp Asn Gln Gln Ala Met Val Arg Arg
             75                  80                  85

gag tct gtg gtc aat ctg gag aac ttc agg aag cag tat gtc cgc agg   583
Glu Ser Val Val Asn Leu Glu Asn Phe Arg Lys Gln Tyr Val Arg Arg
         90                  95                  100

cgg tgg aag ctt tcc ttc agc atc gtg tcc ctg tgc aac cac ctc acc   631
Arg Trp Lys Leu Ser Phe Ser Ile Val Ser Leu Cys Asn His Leu Thr
    105                 110                 115
```

```
cgc tcg ctg atg aag aag gtg cac ctg agg ccg gat gag gac ctg agg   679
Arg Ser Leu Met Lys Lys Val His Leu Arg Pro Asp Glu Asp Leu Arg
120                 125                 130                 135

aac tgt gag agt gac act gag gag gac atc gcc agg agg aaa gcc ctc   727
Asn Cys Glu Ser Asp Thr Glu Glu Asp Ile Ala Arg Arg Lys Ala Leu
                140                 145                 150

cac cca cgg agg agg agc agc acc tcc taactggcct gacctgcagt         774
His Pro Arg Arg Arg Ser Ser Thr Ser
            155                 160

ggccgccagg gaggtctggg cccagcgggg ctcccttctg tgcagacttt tggacccagc 834

tcagcaccag cacccgggcg tcctgagcac tttgcaagag agatgggccc aaggaattca 894

gaagagcttg caggcaagcc aggagaccct gggagctgtg gctgtcttct gtggaggagg 954

ctccagcatt cccaaagctc ttaattctcc ataaaatggg ctttcctctg tctgccatcc 1014

tcagagtctg gggtgggagt gtggacttag gaaaacaata taaaggacat cctcatcatc 1074

acgggggtgaa ggtcagacta aggcagcctt cttcacaggc tgagggggtt cagaaccagc 1134

ctggccaaaa attacaccag agagacagag tcctccccat tgggaacagg gtgattgagg 1194

aaagtgaacc ttgggtgtga gggaccaatc ctgtgacctc ccagaaccat ggaagccagg 1254

acgtcaggct gaccaacacc tcagaccttc tgaagcagcc cattgctggc ccgccatgtt 1314

gtaattttgc tcatttttat taaacttctg gtttacctga tgcttggctt cttttagggc 1374

tacccccatc tcatttcctt tagcccgtgt gcctgtaact ctgaggggggg gcacccagtg 1434

gggtgctgag tgggcagaat ctcagaaggt cctcctgaac cgtccgcgca ggcctgcagt 1494

gggcctgcct cctccttgct tccctaacag gaaggtgtcc agttcaagag aacccaccca 1554

gagactggga gtggtggctc acgcctataa tccctgcgct ttggcagtcc gaggcagggg 1614

aattgcttga actcaggagt tggagaccag cctgggcaac atggcaaaac gcagtctgta 1674

caaaaaatac aaaaaattag ccaggtgtag gggtaggcac ctggcatccc agctactcca 1734

ggggctgagg tgacagcatt gcttaagccc agaaggtcga ggctgcagtg agctgagatc 1794

acgccactgc actccagtct gggtgacaga gagagaccat atccaaaaaa aaaaaaaaaa 1854

gggcggccgc                                                        1864
```

<210> 11
<211> 160
<212> PRT
<213> Homo sapiens

<400> 11

```
Leu Phe Asp Ser Leu Ser Val Val Leu Ser Leu Ser Gly Ala Ser Pro
 1               5                  10                  15

Phe Leu Gly Asp Thr Lys Gln Glu Thr Leu Ala Asn Ile Thr Ala Val
            20                  25                  30

Ser Tyr Asp Phe Asp Glu Glu Phe Phe Ser Gln Thr Ser Glu Leu Ala
        35                  40                  45

Lys Asp Phe Ile Arg Lys Leu Leu Val Lys Glu Thr Arg Lys Arg Leu
    50                  55                  60

Thr Ile Gln Glu Ala Leu Arg His Pro Trp Ile Thr Pro Val Asp Asn
65                  70                  75                  80

Gln Gln Ala Met Val Arg Arg Glu Ser Val Val Asn Leu Glu Asn Phe
                85                  90                  95

Arg Lys Gln Tyr Val Arg Arg Arg Trp Lys Leu Ser Phe Ser Ile Val
            100                 105                 110

Ser Leu Cys Asn His Leu Thr Arg Ser Leu Met Lys Lys Val His Leu
        115                 120                 125

Arg Pro Asp Glu Asp Leu Arg Asn Cys Glu Ser Asp Thr Glu Glu Asp
    130                 135                 140

Ile Ala Arg Arg Lys Ala Leu His Pro Arg Arg Arg Ser Ser Thr Ser
145                 150                 155                 160
```

<210> 12
<211> 480
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(480)

<400> 12

```
tta ttt gat tcc ctg tct gtc gta ctc agc tta agt gga gca tcc cct   48
Leu Phe Asp Ser Leu Ser Val Val Leu Ser Leu Ser Gly Ala Ser Pro
 1               5                  10                  15

ttc ctg gga gac acg aag cag gaa aca ctg gca aat atc aca gca gtg   96
Phe Leu Gly Asp Thr Lys Gln Glu Thr Leu Ala Asn Ile Thr Ala Val
            20                  25                  30

agt tac gac ttt gat gag gaa ttc ttc agc cag acg agc gag ctg gcc   144
Ser Tyr Asp Phe Asp Glu Glu Phe Phe Ser Gln Thr Ser Glu Leu Ala
        35                  40                  45

aag gac ttt att cgg aag ctt ctg gtt aaa gag acc cgg aaa cgg ctc   192
Lys Asp Phe Ile Arg Lys Leu Leu Val Lys Glu Thr Arg Lys Arg Leu
    50                  55                  60
```

```
aca atc caa gag gct ctc aga cac ccc tgg atc acg ccg gtg gac aac   240
Thr Ile Gln Glu Ala Leu Arg His Pro Trp Ile Thr Pro Val Asp Asn
 65                  70                  75                  80

cag caa gcc atg gtg cgc agg gag tct gtg gtc aat ctg gag aac ttc   288
Gln Gln Ala Met Val Arg Arg Glu Ser Val Val Asn Leu Glu Asn Phe
                85                  90                  95

agg aag cag tat gtc cgc agg cgg tgg aag ctt tcc ttc agc atc gtg   336
Arg Lys Gln Tyr Val Arg Arg Arg Trp Lys Leu Ser Phe Ser Ile Val
            100                 105                 110

tcc ctg tgc aac cac ctc acc cgc tcg ctg atg aag aag gtg cac ctg   384
Ser Leu Cys Asn His Leu Thr Arg Ser Leu Met Lys Lys Val His Leu
        115                 120                 125

agg ccg gat gag gac ctg agg aac tgt gag agt gac act gag gag gac   432
Arg Pro Asp Glu Asp Leu Arg Asn Cys Glu Ser Asp Thr Glu Glu Asp
    130                 135                 140

atc gcc agg agg aaa gcc ctc cac cca cgg agg agg agc agc acc tcc   480
Ile Ala Arg Arg Lys Ala Leu His Pro Arg Arg Arg Ser Ser Thr Ser
145                 150                 155                 160
```

<210> 13
<211> 1333
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (2)..(1333)

<400> 13

```
g acg gca tta gcc aaa gaa cta aga gaa ctc cgg att gaa gaa aca aac 49
  Thr Ala Leu Ala Lys Glu Leu Arg Glu Leu Arg Ile Glu Glu Thr Asn
    1               5                  10                  15

cgc cca atg aag aag gtg act gat tac tcc tcc tcc agt gag gag tca   97
Arg Pro Met Lys Lys Val Thr Asp Tyr Ser Ser Ser Ser Glu Glu Ser
            20                  25                  30

gaa agt agc gag gaa gag gag gaa gat gga gag agc gag acc cat gat   145
Glu Ser Ser Glu Glu Glu Glu Glu Asp Gly Glu Ser Glu Thr His Asp
        35                  40                  45

ggg aca gtg gct gtc agc gac ata ccc aga ctg ata cca aca gga gct   193
Gly Thr Val Ala Val Ser Asp Ile Pro Arg Leu Ile Pro Thr Gly Ala
    50                  55                  60

cca ggc agc aac gag cag tac aat gtg gga atg gtg ggg acg cat ggg   241
Pro Gly Ser Asn Glu Gln Tyr Asn Val Gly Met Val Gly Thr His Gly
 65                  70                  75                  80

ctg gag acc tct cat gcg gac agt ttc agc ggc agt att tca aga gaa   289
Leu Glu Thr Ser His Ala Asp Ser Phe Ser Gly Ser Ile Ser Arg Glu
```

```
                    85                  90                  95

gga acc ttg atg att aga gag acg tct gga gag aag aag cga tct ggc   337
Gly Thr Leu Met Ile Arg Glu Thr Ser Gly Glu Lys Lys Arg Ser Gly
            100                 105                 110

cac agt gac agc aat ggc ttt gct ggc cac atc aac ctc cct gac ctg   385
His Ser Asp Ser Asn Gly Phe Ala Gly His Ile Asn Leu Pro Asp Leu
        115                 120                 125

gtg cag cag agc cat tct cca gct gga acc ccg act gag gga ctg ggg   433
Val Gln Gln Ser His Ser Pro Ala Gly Thr Pro Thr Glu Gly Leu Gly
    130                 135                 140

cgc gtc tca acc cat tcc cag gag atg gac tct ggg act gaa tat ggc   481
Arg Val Ser Thr His Ser Gln Glu Met Asp Ser Gly Thr Glu Tyr Gly
145                 150                 155                 160

atg ggg agc agc acc aaa gcc tcc ttc acc ccc ttt gtg gac ccc aga   529
Met Gly Ser Ser Thr Lys Ala Ser Phe Thr Pro Phe Val Asp Pro Arg
                165                 170                 175

gta tac cag acg tct ccc act gat gaa gat gaa gag gat gag gaa tca   577
Val Tyr Gln Thr Ser Pro Thr Asp Glu Asp Glu Glu Asp Glu Glu Ser
            180                 185                 190

tca gcc gca gct ctg ttt act agc gaa ctt ctt agg caa gaa cag gcc   625
Ser Ala Ala Ala Leu Phe Thr Ser Glu Leu Leu Arg Gln Glu Gln Ala
        195                 200                 205

aaa ctc aat gaa gca aga aag att tcg gtg gta aat gta aac cca acc   673
Lys Leu Asn Glu Ala Arg Lys Ile Ser Val Val Asn Val Asn Pro Thr
    210                 215                 220

aac att cgg cct cat agc gac aca cca gaa atc aga aaa tac aag aaa   721
Asn Ile Arg Pro His Ser Asp Thr Pro Glu Ile Arg Lys Tyr Lys Lys
225                 230                 235                 240

cga ttc aac tca gaa ata ctt tgt gca gct ctg tgg ggt gta aac ctt   769
Arg Phe Asn Ser Glu Ile Leu Cys Ala Ala Leu Trp Gly Val Asn Leu
                245                 250                 255

ctg gtg ggg act gaa aat ggc ctg atg ctt ttg gac cga agt ggg caa   817
Leu Val Gly Thr Glu Asn Gly Leu Met Leu Leu Asp Arg Ser Gly Gln
            260                 265                 270

ggc aaa gtc tat aat ctg atc aac cgg agg cga ttt cag cag atg gat   865
Gly Lys Val Tyr Asn Leu Ile Asn Arg Arg Arg Phe Gln Gln Met Asp
        275                 280                 285

gtg cta gag gga ctg aat gtc ctt gtg aca att tca gga aag aag aat   913
Val Leu Glu Gly Leu Asn Val Leu Val Thr Ile Ser Gly Lys Lys Asn
    290                 295                 300

aag cta cga gtt tac tat ctt tca tgg tta aga aac aga ata cta cat   961
Lys Leu Arg Val Tyr Tyr Leu Ser Trp Leu Arg Asn Arg Ile Leu His
305                 310                 315                 320
```

```
aat gac cca gaa gta gaa aag aaa caa ggc tgg atc act gtt ggg gac   1009
Asn Asp Pro Glu Val Glu Lys Lys Gln Gly Trp Ile Thr Val Gly Asp
                325                 330                 335

ttg gaa ggc tgt ata cat tat aaa gtt gtt aaa tat gaa agg atc aaa   1057
Leu Glu Gly Cys Ile His Tyr Lys Val Val Lys Tyr Glu Arg Ile Lys
            340                 345                 350

ttt ttg gtg att gcc tta aag aat gct gtg gaa ata tat gct tgg gct   1105
Phe Leu Val Ile Ala Leu Lys Asn Ala Val Glu Ile Tyr Ala Trp Ala
        355                 360                 365

cct aaa ccg tat cat aaa ttc atg gca ttt aag tct ttt gca gat ctc   1153
Pro Lys Pro Tyr His Lys Phe Met Ala Phe Lys Ser Phe Ala Asp Leu
    370                 375                 380

cag cac aag cct ctg cta gtt gat ctc acg gta gaa gaa ggt caa aga   1201
Gln His Lys Pro Leu Leu Val Asp Leu Thr Val Glu Glu Gly Gln Arg
385                 390                 395                 400

tta aag gtt att ttt ggt tca cac act ggt ttc cat gta att gat gtt   1249
Leu Lys Val Ile Phe Gly Ser His Thr Gly Phe His Val Ile Asp Val
                405                 410                 415

gat tca gga aac tct tat gat atc tac ata cca tct cat att cag ggc   1297
Asp Ser Gly Asn Ser Tyr Asp Ile Tyr Ile Pro Ser His Ile Gln Gly
            420                 425                 430

aat atc act cct cat gct att gtc atc ttg cct aaa                  1333
Asn Ile Thr Pro His Ala Ile Val Ile Leu Pro Lys
        435                 440
```

<210> 14
<211> 444
<212> PRT
<213> Homo sapiens

<400> 14

```
Thr Ala Leu Ala Lys Glu Leu Arg Glu Leu Arg Ile Glu Glu Thr Asn
  1               5                  10                  15

Arg Pro Met Lys Lys Val Thr Asp Tyr Ser Ser Ser Ser Glu Glu Ser
            20                  25                  30

Glu Ser Ser Glu Glu Glu Glu Glu Asp Gly Glu Ser Glu Thr His Asp
        35                  40                  45

Gly Thr Val Ala Val Ser Asp Ile Pro Arg Leu Ile Pro Thr Gly Ala
    50                  55                  60

Pro Gly Ser Asn Glu Gln Tyr Asn Val Gly Met Val Gly Thr His Gly
65                  70                  75                  80

Leu Glu Thr Ser His Ala Asp Ser Phe Ser Gly Ser Ile Ser Arg Glu
                85                  90                  95
```

Gly Thr Leu Met Ile Arg Glu Thr Ser Gly Glu Lys Lys Arg Ser Gly
100 105 110

His Ser Asp Ser Asn Gly Phe Ala Gly His Ile Asn Leu Pro Asp Leu
115 120 125

Val Gln Gln Ser His Ser Pro Ala Gly Thr Pro Thr Glu Gly Leu Gly
130 135 140

Arg Val Ser Thr His Ser Gln Glu Met Asp Ser Gly Thr Glu Tyr Gly
145 150 155 160

Met Gly Ser Ser Thr Lys Ala Ser Phe Thr Pro Phe Val Asp Pro Arg
165 170 175

Val Tyr Gln Thr Ser Pro Thr Asp Glu Asp Glu Glu Asp Glu Glu Ser
180 185 190

Ser Ala Ala Ala Leu Phe Thr Ser Glu Leu Leu Arg Gln Glu Gln Ala
195 200 205

Lys Leu Asn Glu Ala Arg Lys Ile Ser Val Val Asn Val Asn Pro Thr
210 215 220

Asn Ile Arg Pro His Ser Asp Thr Pro Glu Ile Arg Lys Tyr Lys Lys
225 230 235 240

Arg Phe Asn Ser Glu Ile Leu Cys Ala Ala Leu Trp Gly Val Asn Leu
245 250 255

Leu Val Gly Thr Glu Asn Gly Leu Met Leu Leu Asp Arg Ser Gly Gln
260 265 270

Gly Lys Val Tyr Asn Leu Ile Asn Arg Arg Arg Phe Gln Gln Met Asp
275 280 285

Val Leu Glu Gly Leu Asn Val Leu Val Thr Ile Ser Gly Lys Lys Asn
290 295 300

Lys Leu Arg Val Tyr Tyr Leu Ser Trp Leu Arg Asn Arg Ile Leu His
305 310 315 320

Asn Asp Pro Glu Val Glu Lys Lys Gln Gly Trp Ile Thr Val Gly Asp
325 330 335

Leu Glu Gly Cys Ile His Tyr Lys Val Val Lys Tyr Glu Arg Ile Lys
340 345 350

Phe Leu Val Ile Ala Leu Lys Asn Ala Val Glu Ile Tyr Ala Trp Ala
355 360 365

Pro Lys Pro Tyr His Lys Phe Met Ala Phe Lys Ser Phe Ala Asp Leu
370 375 380

Gln His Lys Pro Leu Leu Val Asp Leu Thr Val Glu Glu Gly Gln Arg
385 390 395 400

```
Leu Lys Val Ile Phe Gly Ser His Thr Gly Phe His Val Ile Asp Val
                405                 410                 415

Asp Ser Gly Asn Ser Tyr Asp Ile Tyr Ile Pro Ser His Ile Gln Gly
            420                 425                 430

Asn Ile Thr Pro His Ala Ile Val Ile Leu Pro Lys
        435                 440


<210> 15
<211> 1332
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1332)

<400> 15
acg gca tta gcc aaa gaa cta aga gaa ctc cgg att gaa gaa aca aac   48
Thr Ala Leu Ala Lys Glu Leu Arg Glu Leu Arg Ile Glu Glu Thr Asn
  1               5                  10                  15

cgc cca atg aag aag gtg act gat tac tcc tcc tcc agt gag gag tca   96
Arg Pro Met Lys Lys Val Thr Asp Tyr Ser Ser Ser Ser Glu Glu Ser
            20                  25                  30

gaa agt agc gag gaa gag gag gaa gat gga gag agc gag acc cat gat   144
Glu Ser Ser Glu Glu Glu Glu Glu Asp Gly Glu Ser Glu Thr His Asp
        35                  40                  45

ggg aca gtg gct gtc agc gac ata ccc aga ctg ata cca aca gga gct   192
Gly Thr Val Ala Val Ser Asp Ile Pro Arg Leu Ile Pro Thr Gly Ala
    50                  55                  60

cca ggc agc aac gag cag tac aat gtg gga atg gtg ggg acg cat ggg   240
Pro Gly Ser Asn Glu Gln Tyr Asn Val Gly Met Val Gly Thr His Gly
65                  70                  75                  80

ctg gag acc tct cat gcg gac agt ttc agc ggc agt att tca aga gaa   288
Leu Glu Thr Ser His Ala Asp Ser Phe Ser Gly Ser Ile Ser Arg Glu
                85                  90                  95

gga acc ttg atg att aga gag acg tct gga gag aag aag cga tct ggc   336
Gly Thr Leu Met Ile Arg Glu Thr Ser Gly Glu Lys Lys Arg Ser Gly
            100                 105                 110

cac agt gac agc aat ggc ttt gct ggc cac atc aac ctc cct gac ctg   384
His Ser Asp Ser Asn Gly Phe Ala Gly His Ile Asn Leu Pro Asp Leu
        115                 120                 125

gtg cag cag agc cat tct cca gct gga acc ccg act gag gga ctg ggg   432
Val Gln Gln Ser His Ser Pro Ala Gly Thr Pro Thr Glu Gly Leu Gly
    130                 135                 140
```

```
cgc gtc tca acc cat tcc cag gag atg gac tct ggg act gaa tat ggc   480
Arg Val Ser Thr His Ser Gln Glu Met Asp Ser Gly Thr Glu Tyr Gly
145                 150                 155                 160

atg ggg agc agc acc aaa gcc tcc ttc acc ccc ttt gtg gac ccc aga   528
Met Gly Ser Ser Thr Lys Ala Ser Phe Thr Pro Phe Val Asp Pro Arg
                165                 170                 175

gta tac cag acg tct ccc act gat gaa gat gaa gag gat gag gaa tca   576
Val Tyr Gln Thr Ser Pro Thr Asp Glu Asp Glu Glu Asp Glu Glu Ser
            180                 185                 190

tca gcc gca gct ctg ttt act agc gaa ctt ctt agg caa gaa cag gcc   624
Ser Ala Ala Ala Leu Phe Thr Ser Glu Leu Leu Arg Gln Glu Gln Ala
        195                 200                 205

aaa ctc aat gaa gca aga aag att tcg gtg gta aat gta aac cca acc   672
Lys Leu Asn Glu Ala Arg Lys Ile Ser Val Val Asn Val Asn Pro Thr
    210                 215                 220

aac att cgg cct cat agc gac aca cca gaa atc aga aaa tac aag aaa   720
Asn Ile Arg Pro His Ser Asp Thr Pro Glu Ile Arg Lys Tyr Lys Lys
225                 230                 235                 240

cga ttc aac tca gaa ata ctt tgt gca gct ctg tgg ggt gta aac ctt   768
Arg Phe Asn Ser Glu Ile Leu Cys Ala Ala Leu Trp Gly Val Asn Leu
                245                 250                 255

ctg gtg ggg act gaa aat ggc ctg atg ctt ttg gac cga agt ggg caa   816
Leu Val Gly Thr Glu Asn Gly Leu Met Leu Leu Asp Arg Ser Gly Gln
            260                 265                 270

ggc aaa gtc tat aat ctg atc aac cgg agg cga ttt cag cag atg gat   864
Gly Lys Val Tyr Asn Leu Ile Asn Arg Arg Arg Phe Gln Gln Met Asp
        275                 280                 285

gtg cta gag gga ctg aat gtc ctt gtg aca att tca gga aag aag aat   912
Val Leu Glu Gly Leu Asn Val Leu Val Thr Ile Ser Gly Lys Lys Asn
    290                 295                 300

aag cta cga gtt tac tat ctt tca tgg tta aga aac aga ata cta cat   960
Lys Leu Arg Val Tyr Tyr Leu Ser Trp Leu Arg Asn Arg Ile Leu His
305                 310                 315                 320

aat gac cca gaa gta gaa aag aaa caa ggc tgg atc act gtt ggg gac  1008
Asn Asp Pro Glu Val Glu Lys Lys Gln Gly Trp Ile Thr Val Gly Asp
                325                 330                 335

ttg gaa ggc tgt ata cat tat aaa gtt gtt aaa tat gaa agg atc aaa  1056
Leu Glu Gly Cys Ile His Tyr Lys Val Val Lys Tyr Glu Arg Ile Lys
            340                 345                 350

ttt ttg gtg att gcc tta aag aat gct gtg gaa ata tat gct tgg gct  1104
Phe Leu Val Ile Ala Leu Lys Asn Ala Val Glu Ile Tyr Ala Trp Ala
        355                 360                 365

cct aaa ccg tat cat aaa ttc atg gca ttt aag tct ttt gca gat ctc  1152
```

```
Pro Lys Pro Tyr His Lys Phe Met Ala Phe Lys Ser Phe Ala Asp Leu
    370                 375                 380

cag cac aag cct ctg cta gtt gat ctc acg gta gaa gaa ggt caa aga   1200
Gln His Lys Pro Leu Leu Val Asp Leu Thr Val Glu Glu Gly Gln Arg
385                 390                 395                 400

tta aag gtt att ttt ggt tca cac act ggt ttc cat gta att gat gtt   1248
Leu Lys Val Ile Phe Gly Ser His Thr Gly Phe His Val Ile Asp Val
                405                 410                 415

gat tca gga aac tct tat gat atc tac ata cca tct cat att cag ggc   1296
Asp Ser Gly Asn Ser Tyr Asp Ile Tyr Ile Pro Ser His Ile Gln Gly
            420                 425                 430

aat atc act cct cat gct att gtc atc ttg cct aaa                  1332
Asn Ile Thr Pro His Ala Ile Val Ile Leu Pro Lys
        435                 440
```